

Anti-CD3 Light Chain Variable Region

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GACTTTATGCTTACTCAGCCCCACTCTGTGTCTGAGTCTCCCGAAAGACAGTCATTATT 60
D F M L T Q P H S V S E S P G K T V I I 20

TCTTGACACTCAGCTCTGGTAACATAGAAAACAACACTATGTGCACTGGTACCAAGAAAG 120
S C T L S S G N I E N N Y V H W Y Q Q R 40

CCGGGAAGAGCTCCCACTCGTGATTTTCGATGATGATAAGAGACCCGGATGGTGTCCT 180
P G R A P T L V I F D D D K R P D G V P 60

GACAGGTTCTCTGGCTCCATTGACAGGTCTTCCAACCTCAGCCTCCCTGACAATCAGTGGT 240
D R F S G S I D R S S N S A S L T I S G 80

CTGCAAACTGAAGATGAAGCTGACTACTACTGTCACTTCTTATGTTAGTAGTTTAAATGTT 300
L Q T E D E A D Y Y C H S Y V S S F N V 100

TTCGGCGGTGGAACAAAGCTCACTGTCCTT 330 (SEQ ID NO:16)
F G G G T K L T V L 110 (SEQ ID NO:15)
  
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Figure 1

Anti-CD3 Heavy Chain Variable Region

CAGGTCCAATTGCAGGAGTCTGGGGCGGTTAGTGAGCCTGGAAGGTCCATGAAACTC	60
Q V Q L Q E S G G G L V Q P G R S M K L	20
TCCTGTGCAGCCTCAGGATTCACTTTCAGTAGCTTTCCAATGGCTGGTCCGCCAGGCT	120
S C A A S G F T F S S F P M A W V R Q A	40
CCAAAGAAGGTCTGGAGTGGGTCGCAACCATTAGTACTAGTGGTAGAACTTACTAT	180
P K K G L E W V A T I S T S G G R T Y Y	60
CGAGACTCCGTGAAGGGCGATTCACTATCTCCAGAGATAATGGGAAAGCATCCTATAC	240
R D S V K G R F T I S R D N G K S I L Y	80
CTGCAATGAATAGTCTGAGGTCTGAGGACACGGCCACTTATTACTGTTCAGATTTCCGG	300
L Q M N S L R S E D T A T Y Y C S R F R	100
CAGTACAGTGGTGGCTTTGATTACTGGGGCCAAGGACCGGTCAACCGTCAGCTCA	357 (SEQ ID NO:18)
Q Y S G G F D Y W G Q G T T V T V S S	119 (SEQ ID NO:17)

Figure 2

SEQUENCE LIST

Aglycosylated Human IgG1 Constant Region

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GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG
A S T K G P S V F P L A P S S K S T S G
GGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAAACCGGTGACGGTGTCTG
G T A A L G C L V K D Y F P E P V T V S
TGGAACCTCAGGGCGCCCTGACCAGCGGGCGTGACACACCTTCCCCGGCTGTCTACAGTCTCTCA
W N S G A L T S G V H T F P A V L Q S S
GGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACC
G L Y S L S S V V T V P S S S L G T Q T
TACATCTGCAACGTGAATCACAAAGCCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCC
Y I C N V N H K P S N T K V D K K V E P
AAATCTTGACAAAACTCACACATGCCACCGTGCCAGCACCTGAACCTCCTGGGGGA
K S C D K T H T C P P C P A P E L L G G
CCGTGAGTCTTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCT
P S V F L F P P K P K D T L M I S R T P
GAGGTACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGG
E V T C V V V D V S H E D P E V K F N W

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Figure 3A

SEQUENCE # 44209001

TACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACGCC
Y V D G V E V H N A K T K P R E E Q Y A 297

AGCACGTACCGTGTGGTCAGCGTCCCTCACCGTCCCTGCACAGGACTGGCTGAATGGCAAG
S T Y R V V S V L T V L H Q D W L N G K

GAGTACAAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAAACCATCTCC
E Y K C K V S N K A L P A P I E K T I S

AAAGCCAAAGGCGAGCCCCGAGAACCAAGGTGTACACCCCTGCCCCCATCCCGGATGAG
K A K G Q P R E P Q V Y T L P P S R D E

CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATC
L T K N Q V S L T C L V K G F Y P S D I

GCCGTGGAGTGGAGAGCAATGGGCAGCCCGGAGAACAACTACAAGACCCACGCCCTCCCGTG
A V E W E S N G Q P E N N Y K T T P P V

CTGGACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGACAAAGAGCAGGTGG
L D S D G S F F L Y S K L T V D K S R W

CAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG
Q Q G N V F S C S V M H E A L H N H Y T

CAGAAAGAGCCTCTCCCTGTCTCCGGGTAATGA (SEQ ID NO:26)
Q K S L S L S P G K Op (SEQ ID NO:25)

Figure 3B